

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/612,468B
Source: 1FW/6
Date Processed by STIC: 1/10/07

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06



IFW16

RAW SEQUENCE LISTING

DATE: 01/10/2007

PATENT APPLICATION: US/10/612,468B

TIME: 09:43:35

Input Set : A:\D6622SEQ.txt

Output Set: N:\CRF4\01102007\J612468B.raw

3 <110> APPLICANT: Zhang, Jingwu Z.
 4 Ho, Walter Kowk Keung
 5 Zhang, Dongqing
 6 Sun, Wei
 8 <120> TITLE OF INVENTION: T Cell Receptor CDR3 Sequence and Methods for
 9 Detecting and Treating Rheumatoid Arthritis
 11 <130> FILE REFERENCE: D6622
 13 <140> CURRENT APPLICATION NUMBER: US 10/612,468B
 14 <141> CURRENT FILING DATE: 2003-07-02
 16 <150> NUMBER OF SEQ ID NOS: 168

ERRORED SEQUENCES

416 <210> SEQ ID NO: 29
 417 <211> LENGTH: 21
 418 <212> TYPE: DNA
 419 <213> ORGANISM: Artificial Sequence
 421 <220> FEATURE:
 422 <221> NAME/KEY: primer_bind
 423 <223> OTHER INFORMATION: reverse primer specific for TCR BV11 used in real-time
 424 PCR analysis
 426 <400> SEQUENCE: 29 atgtgagggc ctggcagact c 21

see pp 1-3
 Does Not Comply
 Corrected Diskette Needed

688 <210> SEQ ID NO: 50
 689 <211> LENGTH: 23
 E--> 690 ~~<223>~~ DNA *<212>*
 691 <213> ORGANISM: Artificial Sequence
 693 <220> FEATURE:
 694 <221> NAME/KEY: primer_bind
 695 <223> OTHER INFORMATION: forward primer specific for TCR BV22 used in real-time
 696 PCR analysis
 698 <400> SEQUENCE: 50
 699 cacagatggg acaggaagtg atc 23
 727 <210> SEQ ID NO: 53
 728 <211> LENGTH: 21
 729 <212> TYPE: DNA
 730 <213> ORGANISM: Artificial Sequence
 732 <220> FEATURE: *<221>*
 E--> 733 ~~<21>~~ primer_bind
 734 <223> OTHER INFORMATION: reverse primer specific for TCR BV23 used in real-time
 735 time PCR analysis

RAW SEQUENCE LISTING

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PATENT APPLICATION: US/10/612,468B

TIME: 09:43:35

Input Set : A:\D6622SEQ.txt

Output Set: N:\CRF4\01102007\J612468B.raw

737 <400> SEQUENCE: 53
 738 cagctccaag gagctcatgt t 21
 740 <210> SEQ ID NO: 54
 741 <211> LENGTH: 24
 742 <212> TYPE: DNA
 743 <213> ORGANISM: Artificial Sequence
 745 <220> FEATURE:
 746 <221> NAME/KEY: primer_bind
 747 <223> OTHER INFORMATION: forward primer specific for TCR BV24 used in real-time
 748 PCR analysis *Insert a hard return*
 750 <400> SEQUENCE: 54 ccaagataacc aggttaccca gttt 24

1271 <210> SEQ ID NO: 93
 1272 <211> LENGTH: 20
 1273 <212> TYPE: PRT
 1274 <213> ORGANISM: Homo sapiens
 1276 <220> FEATURE:
 1277 <221> NAME/KEY: Domain
 1278 <223> OTHER INFORMATION: CDR3 amino acid sequence of BV16 clonotype derived
 1279 from ST specimen of RA patient

1281 <400> SEQUENCE: 93
 1282 Tyr Phe Cys Ala Ser Ser Gln Ala Asp Gly Thr His Tyr Glu Gln
 1283 5 10 15
 1284 Phe Phe Gly Pro Gly

E--> 1285 ~~20~~ 20 *misaligned amino acid number*

1287 <210> SEQ ID NO: 94

1288 <211> LENGTH: 60 } <2127

E--> 1289 ~~(12)~~ DNA

1290 <213> ORGANISM: Artificial Sequence

1292 <220> FEATURE:

1293 <221> NAME/KEY: CDS

1294 <223> OTHER INFORMATION: CDR3 nucleic acid sequence of BV16 clonotype derived
 1295 from ST specimen of RA patients

1298 <400> SEQUENCE: 94

1299 tattttctgtg ccagcagcca agctgacggg acccattacg agcagtactt 50

1300 cgggccgggc 60

1968 <210> SEQ ID NO: 140

1969 <211> LENGTH: 57 } <2127

E--> 1970 ~~(21)~~ DNA

1971 <213> ORGANISM: Artificial Sequence

1973 <220> FEATURE:

1974 <221> NAME/KEY: CDS

1975 <223> OTHER INFORMATION: CDR3 nucleic acid sequence of BV14 clonotype derived
 1976 from ST specimen of RA patients

1978 <400> SEQUENCE: 140

1979 tactttctgtg ccagcagttt atcttcgaca gggaggaggc agtacttcgg gccgggc 57

2371 <210> SEQ ID NO: 168

RAW SEQUENCE LISTING

DATE: 01/10/2007

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TIME: 09:43:35

Input Set : A:\D6622SEQ.txt

Output Set: N:\CRF4\01102007\J612468B.raw

2372 <211> LENGTH: 54

2373 <212> TYPE: DNA

2374 <213> ORGANISM: Artificial Sequence

2376 <220> FEATURE:

2377 <221> NAME/KEY: CDS

2378 <223> OTHER INFORMATION: CDR3 nucleic acid sequence of BV14 clonotype derived

2379 from ST specimen of RA patients

2381 <400> SEQUENCE: 168

2382 tacttctgtg ccagcagttc cctcgctact gctgaagctt tctttggaca aggc 54

E--> 2383 ??

E--> 2385 ??

E--> 2387 ??

E--> 2389 ??

delete

VERIFICATION SUMMARY

DATE: 01/10/2007

PATENT APPLICATION: US/10/612,468B

TIME: 09:43:36

Input Set : A:\D6622SEQ.txt

Output Set: N:\CRF4\01102007\J612468B.raw

L:426 M:301 E: (44) No Sequence Data was Shown, SEQ ID:29
L:426 M:252 E: No. of Seq. differs, <211> LENGTH:Input:21 Found:0 SEQ:29
L:690 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
L:698 M:282 E: Numeric Field Identifier Missing, <212> is required.
L:733 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
L:750 M:301 E: (44) No Sequence Data was Shown, SEQ ID:54
L:750 M:252 E: No. of Seq. differs, <211> LENGTH:Input:24 Found:0 SEQ:54
L:1285 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:93
L:1289 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
L:1298 M:282 E: Numeric Field Identifier Missing, <212> is required.
L:1970 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
L:1978 M:282 E: Numeric Field Identifier Missing, <212> is required.
L:2383 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:2385 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:168
L:2385 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:2387 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:168
L:2387 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:2389 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:168
L:2389 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1